Corrigendum

In the article by M. Shinohara, D. K. Bishop, and A. Shinohara (Genetics, 213: 1255–1269) entitled “Distinct Functions in Regulation of Meiotic Crossovers for DNA Damage Response Clamp Loader Rad24 (Rad17) and Mec1(ATR) Kinase,” errors were made in preparing Table 1, Table 3, and Table 4. These errors had no impact on any of the conclusions of the paper. The errors involved data entry and statistical analysis. *P*-values that were significantly altered, with respect to the conventional threshold of 0.05, are underlined in the corrected versions of Table 1, Table 3, and Table 4 presented here.

First, the original version of Table 3 contained minor typographical errors (Table 3, footnote “*f*”) and also a significant data entry error for the number of nonparental ditypes (NPDs) expected from the value obtained from the Papazian equation (NPDe) for the *HIS4-MAT* interval data in wild-type. The corrected NPDe value and the corresponding *P*-value are indicated by footnote “*g*” (Table 3). Correcting this data entry error strengthens the original conclusion that the mutants display significant defects in crossover interference compared with wild-type.

Table 1 Genetic analysis of meiotic recombination on chromosome V in *rad24* and *mec1* mutants

	Intervals	PD	TT	NPD _o	Total	Papazian NPDe	cM (SE) ^a	NPD ratio ^b	P-value for difference from WT ^c	Papazian P-value for NPD ratio <1 ^d	BW P-value ^e
WT	<i>CAN1-URA3</i>	313	744	29	1086	121	42.3 ± 1.5	NA ^f	—	NA ^f	0
	<i>URA3-HOM3</i>	343	696	43	1082	135	44.1 ± 1.7	0.32 ± 0.06	—	1.7×10^{-23}	0
	<i>HOM3-TRP2</i>	824	240	3	1067	8.0	12.1 ± 0.8	0.37 ± 0.22	—	0.0024*	0.23
<i>rad24</i>	<i>CAN1-URA3</i>	804	358	22	1184	17.3	20.7 ± 1.3 (0.49)	1.27 ± 0.28	$<2.2 \times 10^{-16}$	0.81	0.57
	<i>URA3-HOM3</i>	737	420	22	1179	25.3	23.4 ± 1.3 (0.53)	0.87 ± 0.19	$<2.2 \times 10^{-16}$	0.26	0.87
	<i>HOM3-TRP2</i>	1019	146	2	1167	2.5	6.8 ± 0.6 (0.56)	0.80 ± 0.57	6.8×10^{-10}	0.37	0.98
<i>mec1 sml1-X</i>	<i>CAN1-URA3</i>	496	524	48	1068	52.2	38.0 ± 1.9 (0.90)	0.92 ± 0.15	$<2.2 \times 10^{-16}$	0.31	0.91
	<i>URA3-HOM3</i>	418	562	69	1049	66.3	46.5 ± 2.2 (1.05)	1.04 ± 0.14	1.2×10^{-6}	0.59	0.96
	<i>HOM3-TRP2</i>	719	287	17	1023	12.6	19.0 ± 1.3 (1.57)	1.35 ± 0.34	2.8×10^{-5}	0.83	0.50

P-values followed by an asterisk are significantly different from those presented for the flawed Papazian analysis in the original paper. PD, number of parental ditypes; TT, number of tetratypes; NPD_o, number of observed NPDs; NPDe, number of NPDs expected from Papazian equation; NPD, nonparental ditype; WT, wild type; BW, a better way; NA, not applicable.

^a Map distances and NPD ratios with SE were calculated using the Stahl laboratory online tools. Numbers in parentheses following each mutant map distance are the ratios of mutant map distance/WT map distance.

^b NPD ratio = NPD_o/NPDe, with NPDe calculated using the Papazian equation.

^c Differences between the WT and mutant were calculated via Fisher's exact test implemented by R software.

^d *P*-values for the significance of NPDe ratios from Papazian being <1, i.e., for rejecting the null hypothesis that NPD observed is not significantly different from NPD expected. To test whether the NPD observed are significantly smaller than the NPD expected using the Papazian ratio, we consider whether the ratio is significantly <1. The test statistic is the ratio − 1, standardized by the SE as given at <https://elizabethhousworth.com/StahlLabOnlineTools/EquationsMapDistance.html>. If the SE is much smaller than the NPD ratio, then this statistic is approximately normally distributed. The *P*-values provided come from the lower tail of a normal distribution. *P*-values followed by an asterisk are significantly different from those presented for the flawed Papazian analysis in the original paper.

^e *P*-values for BW were calculated using the exact multinomial test with the EMT package in R and the default settings. With respect to the conventional threshold of *P* = 0.05, there are no significant differences between the list of intervals displaying significant interference as determined by BW here, and the corresponding list from the flawed Papazian analysis in the original paper. All values obtained by BW are in agreement with the originally published values for the significance of interference, with respect to the conventional threshold of *P* = 0.05.

^f Papazian analysis cannot be applied in situations where TT frequencies exceed two-thirds of the total.

Table 3 Genetic analysis of meiotic recombination on chromosome III in *rad24* and *mec1* mutants

	Intervals	PD	TT	NPD _o	Total	Papazian NPDe	cM (SE) ^a	NPD ratio ^b	P-value for difference from WT ^c	Papazian P-value for NPD ratio <1 ^d	BW P-value ^e
WT	HML-URA3	1013 ^f	286	2	1301	9.1	11.5 ^f ± 0.7	0.22 ± 0.16	—	1.9 × 10 ⁻⁷	0.04
	URA3-LEU2	908	312	7	1227	12.1	14.4 ± 0.9	0.58 ± 0.22	—	0.033*	0.41
	LEU2-HIS4	1173	55	0	1228	0.4	2.2 ± 0.3	0	—	NA	0.92
	HIS4-MAT	533	712	49	1294	88.9 ^g	38.9 ± 1.6	0.55 ± 0.09	—	1.8 × 10 ^{-16g}	0.021 ^g
<i>rad24</i>	HML-URA3	1191	104	1	1296	1.2	4.2 ± 0.4 (0.37)	0.91 ± 0.91	<2.2 × 10 ⁻¹⁶	0.46	0.99
	URA3-LEU2	1069	125	2	1196	1.8	5.7 ± 0.6 (0.38)	1.14 ± 0.81	<2.2 × 10 ⁻¹⁶	0.56	0.88
	LEU2-HIS4	1182	15 ^f	0	1197	0.02	0.56 ± 0.4 (0.27)	0	1.4 × 10 ⁻⁶	NA	0.88
	HIS4-MAT	734	500	36	1270	34.8	28.2 ± 1.5 (0.72)	1.03 ± 0.18	3.5 × 10 ⁻¹⁶	0.56	0.90
<i>mec1 sml1-X</i>	HML-URA3	1095	90	2	1187	0.95	4.3 ± 0.5 (0.38)	2.22 ± 1.58	<2.2 × 10 ⁻¹⁶	0.77	0.38
	URA3-LEU2	896	190	5	1091	4.70	10.1 ± 0.83 (0.68)	1.06 ± 0.48	8.0 × 10 ⁻⁶	0.54	0.95
	LEU2-HIS4	1084	22	0	1106	0.1	0.99 ± 0.21 (0.45)	0	7.1 × 10 ⁻⁴	NA	0.96
	HIS4-MAT	551	559	52	1162	53.8	37.5 ± 1.8 (0.95)	0.97 ± 0.15	2.8 × 10 ⁻³	0.42	0.99
<i>mec1-kd sml1-X</i>	HML-URA3	1077	177	2	1256*	3.4	7.5 ± 0.6 (0.70)	0.58 ± 0.41	4.3 × 10 ⁻⁷	0.15	0.88
	URA3-LEU2	826	234	6	1066	7.6	12.7 ± 0.9 (0.85)	0.79 ± 0.33	0.14 ^h	0.27	0.93
	LEU2-HIS4	1043	40	0	1083	0.2	1.9 ± 0.29 (0.82)	0	0.4 ^h	NA	0.95
	HIS4-MAT	441	639	78	1158	80.2	47.8 ± 2.1 (1.22)	0.97 ± 0.13	2.8 × 10 ⁻³	0.43	0.99

PD, number of parental ditypes; TT, number of tetratypes; NPD_o, number of observed NPDs; NPDe, number of NPDs expected from Papazian equation; NPD, nonparental ditype; WT, wild type; BW, a better way; NA, not applicable.

^a Map distances and NPD ratios with SE were calculated using the Stahl laboratory online tools. Numbers in parentheses following each mutant map distance are the ratios of mutant map distance/WT map distance.

^b NPD ratio = NPD_o/NPDe, with NPDe calculated using the Papazian equation.

^c Differences between the WT and mutant were calculated via Fisher's exact test implemented by R software.

^d P-values for the significance of NPDe ratios from Papazian being <1, i.e., for rejecting the null hypothesis that NPD observed is not significantly different from NPD expected.

To test whether the NPD observed are significantly smaller than the NPD expected using the Papazian ratio, we consider whether the ratio is significantly <1. The test statistic is the ratio - 1, standardized by the SE as given at <https://elizabethhousworth.com/StahlLabOnlineTools/EquationsMapDistance.html>. If the SE is much smaller than the NPD ratio, then this statistic is approximately normally distributed. The P-values provided come from the lower tail of a normal distribution. P-values followed by an asterisk are significantly different from those presented for the flawed Papazian analysis in the original paper.

^e P-values for BW were calculated using the exact multinomial test with the EMT package in R and the default settings. With respect to the conventional threshold of $P = 0.05$, there are no significant differences between the list of intervals displaying significant interference as determined by BW here, and the corresponding list from the flawed Papazian analysis in the original paper. All values obtained by BW are in agreement with the originally published values for the significance of interference, with respect to the conventional threshold of $P = 0.05$.

^f Minor typographical errors in the original paper are corrected here.

^g A major data recording error in the original paper is corrected here. The original entry for NPD expected from the Papazian equation was given as 45.8. This typographical error obscured the evidence for interference in this interval for WT. As a result, this error also obscured the evidence that the mutants display interference defects in this interval compared with WT. Therefore, correcting this error strengthens the conclusion in the paper that the mutants display defects in interference. The corrected NPDe and the corresponding P-values are given.

^h Two P-values for differences between *mec1-kd* and WT data were erroneously reported to be significant (3.6×10^{-8} for URA3-LEU2 and 3.0×10^{-6} for LEU2-HIS4). Correcting these errors (underlined, in bold) reveals that the defects conferred by the mutant are not as extensive as originally implied; a significant defect was detected in only two of four intervals, rather than in four of four.

Second, the chi square test function of Microsoft Excel software was applied incorrectly in the original analysis. The resulting errors included, but were not limited to, failure to adhere to the conventional restriction for chi square tests that no more than 25% of cells may have expected values of <5. In the corrected tables shown here, multinomial exact tests are used to determine whether data for mutant strains differ significantly from that for wild-type (footnote “^e”). The only important impact of these errors is that the defects detected for the two *mec1* alleles are not as extensive as previously indicated; the conclusion that both *mec1-1* and *mec1-kd* mutants display significant defects, and the conclusion that the defects displayed by *mec1-kd* are less extensive than those displayed by *mec1-1*, remain valid.

Finally, we inadvertently used the outdated method of Papazian (1952) to obtain evidence for crossover interference from NPD ratios and also used an invalid method to determine P-values from the Papazian NPDe values. We have now replaced Papazian analysis with the more statistically accurate method referred to as “a better way” (BW; Stahl 2008; see rightmost column in each table; footnote “^e”). We also show the results of properly applied Papazian analysis (columns titled “Papazian P-value for NPD ratio <1”; footnote “^d”). Note that there are four cases (indicated with asterisks) where, had we properly analyzed NPDe from Papazian, we would have concluded there was significant interference, but BW analysis leads us to conclude that the data do not provide evidence for interference. However, there are no cases in which the P-values that were published, and those calculated here for the BW, differ with respect to meeting or failing to meet the conventional threshold for significance of 0.05. Thus, correcting the errors made in assessing interference from NPD ratios has no impact on any of the conclusions of the paper. We apologize for any confusion caused by these errors.

Table 4 Genetic analysis of meiotic recombination on chromosome VII in *rad24* and *mec1* mutants

	Intervals	PD	TT	NPD _o	Total	Papazian NPD _e	cM (SE) ^a	NPD ratio ^b	P-value for difference from WT ^c	Papazian P-value for NPD ratio <1 ^d	BW P-value ^e
Wild type	CUP2-MET13	531	630	17	1178	74.1	31.1 ± 1.2	0.23 ± 0.06	—	2.3 × 10 ⁻³⁷	0
	MET13-CYH2	964	273	0	1237	8.9	11.0 ± 0.6	0	—	NA	0.0015
	CYH2-TRP5	483	756	45	1284	111	40 ± 1.5	0.41 ± 0.07	—	1.3 × 10 ⁻¹⁵	0
	TRP5-ADE6	387	798	91	1276	139	52.7 ± 2.0	0.65 ± 0.09	—	5.3 × 10 ⁻⁴	0.0231
<i>rad24</i>	CUP2-MET13	645	482	42	1169	36.0	31.4 ± 1.7 (0.33)	1.17 ± 0.19	8.8 × 10 ⁻¹⁰	0.78	0.69
	MET13-CYH2	986	236	3	1225	6.6	10.4 ± 0.7 (0.94)	0.46 ± 0.26	0.04	0.022*	0.44
	CYH2-TRP5	499	682	81	1262	81.9	46.3 ± 2.0 (1.16)	0.99 ± 0.13	8.1 × 10 ⁻⁴	0.47	1.0
	TRP5-ADE6	453	693	95	1241	89.4	50.9 ± 2.1 (0.97)	1.06 ± 0.13	2.2 × 10 ⁻³	0.66	0.90
<i>mec1 sml1-X</i>	CUP2-MET13	414	576	43	1033	74	40.4 ± 1.8 (1.30)	0.58 ± 0.10	7.7 × 10 ⁻⁵	8.1 × 10 ⁻⁵	0.014
	MET13-CYH2	830	279	6	1115	10.6	14.1 ± 0.9 (1.28)	0.57 ± 0.23	4.0 × 10 ⁻³	0.034	0.44
	CYH2-TRP5	351	695	95	1141	112	55.4 ± 2.3 (1.39)	0.85 ± 0.11	5.9 × 10 ⁻⁸	0.14	0.60
	TRP5-ADE6	326	674	108	1108	108	59.7 ± 2.5 (1.13)	1.0 ± 0.12	0.07 ^f	0.51	1.0
<i>mec1-kd sml1-X</i>	CUP2-MET13	389	615	45	1049	89.0	42.2 ± 1.8 (1.35)	0.51 ± 0.08	9.5 × 10 ⁻⁷	1.5 × 10 ⁻⁷	0
	MET13-CYH2	805	305	5	1115	12.9	15.0 ± 0.9 (1.36)	0.39 ± 0.17	3.1 × 10 ⁻⁴	3.0 × 10 ^{-4*}	0.083
	CYH2-TRP5	300	773	97	1170	173	57.9 ± 2.2 (1.45)	0.56 ± 0.09	3.3 × 10 ⁻¹³	4.4 × 10 ⁻⁴	0.0056
	TRP5-ADE6	299	708	112	1119	129	61.7 ± 2.5 (1.17)	0.87 ± 0.11	0.014	0.19	0.71

PD, number of parental ditypes; TT, number of tetratypes; NPD_o, number of observed NPDs; NPD_e, number of NPDs expected from Papazian equation; NPD, nonparental ditype; WT, wild type; BW, a better way; NA, not applicable.

^a Map distances and NPD ratios with SE were calculated using the Stahl laboratory online tools. Numbers in parentheses following each mutant map distance are the ratios of mutant map distance/WT map distance.

^b NPD ratio = NPD_o/NPD_e, with NPD_e calculated using the Papazian equation.

^c Differences between the WT and mutant were calculated via Fisher's exact test implemented by R software.

^d P-values for the significance of NPD_e ratios from Papazian being <1, i.e., for rejecting the null hypothesis that NPD observed is not significantly different from NPD expected.

To test whether the NPD observed are significantly smaller than the NPD expected using the Papazian ratio, we consider whether the ratio is significantly <1. The test statistic is the ratio - 1, standardized by the SE as given at <https://elizabethhousworth.com/StahlLabOnlineTools/EquationsMapDistance.html>. If the SE is much smaller than the NPD ratio, then this statistic is approximately normally distributed. The P-values provided come from the lower tail of a normal distribution. P-values followed by an asterisk are significantly different from those presented for the flawed Papazian analysis in the original paper.

^e P-values for BW were calculated using the exact multinomial test with the EMT package in R and the default settings. With respect to the conventional threshold of $P = 0.05$, there are no significant differences between the list of intervals displaying significant interference as determined by BW here, and the corresponding list from the flawed Papazian analysis in the original paper. All values obtained by BW are in agreement with the originally published values for the significance of interference, with respect to the conventional threshold of $P = 0.05$.

^f A P-value for the difference between *mec1* and WT data was erroneously reported to be significant ($P = 6.4 \times 10^{-17}$). Correcting this error reveals that the defects conferred by *mec1* are not as extensive as originally reported: a significant defect was detected in only three of four intervals, rather than in four of four.

Literature Cited

- Papazian, H., 1952 The analysis of tetrad data. *Genetics* 37: 175–188.
 Stahl, F. W., 2008 On the “NPD ratio” as a test for crossover interference. *Genetics* 179: 701–704. <https://doi.org/10.1534/genetics.108.086918>